

**IN THE SPECIFICATION:**

**Please amend the paragraph beginning on page 30, line 6, as follows:**

The polyadenylation signal AATAAATAAA (SEQ ID NO: 58) is at nucleotide position ~~1451~~1574 to ~~1460~~1583 of SEQ ID NO: 12; the coding sequences of NR6.1 (SEQ ID NO:12) and NR6.2 (SEQ ID NO:14) are identical to ~~the codon~~nucleotide 1223 encoding Q407, ~~the~~which represents the end of an exon. NR6.1 splices out an exon present only in NR6.2 and uses a different reading frame for the final exon which is shared with NR6.2; this corresponds to amino acids VLPACL at amino acid residue positions 408-413 of SEQ ID NO: 13. The region of 3'-untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide ~~1240~~1363 to ~~1475~~1598 of SEQ ID NO: 12. The WSXWS motif is at amino acid residues 330 to 334 of SEQ ID NO: 13.

**Please amend the paragraph beginning on page 30, line 15, as follows:**

The polyadenylation signal AATAAAATAAATAAA (SEQ ID NO: 58) is at nucleotide positions ~~1494~~1618 to ~~1503~~1627 of SEQ ID NO: 14. The WSXWS motif is at amino acid residues 330 to 334 of SEQ ID NO: 15. NR6.1 and NR6.2 are identical to ~~the codon~~nucleotide 1223 encoding Q407 which represents the end of an exon. NR6.2 splices in an exon beginning at ~~amino acid residue D408~~, nucleotide ~~1224~~1348 and ends at ~~residue G422~~, nucleotide ~~1264~~1388 of SEQ ID NO: 14 (corresponding to the coding sequence for amino acid residue D408 to residue G422 of SEQ ID NO: 15). The region of 3' untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide position ~~1283~~1407 to ~~1517~~1641 of SEQ ID NO: 14.

**Please amend the paragraph beginning on page 30, line 22, as follows:**

~~The nucleotide and amino acid numbering corresponds to SEQ ID NO:12 and 14.~~ The WSXWS motif is at amino acid residues ~~330 to 334~~24-28 of SEQ ID NO: 17. The polyadenylation signal

AATAAATAAA (SEQ ID NO: 58) is from nucleotide ~~1781863~~ to ~~1780872~~ of SEQ ID NO: 16. NR6.1, NR6.2 and Amino acids 1-101 of NR6.3 (SEQ ID NO: 17) are identical to amino acids 307-407 of NR 6.1 (SEQ ID NO: 13) and NR6.2 (SEQ ID NO: 15). ~~nucleotide-1223~~ The codon encoding Q407 of SEQ ID NO: 13 or Q101 of SEQ ID NO: 17, ~~this~~ represents the end of an exon. NR6.3 fails to splice from this position and, therefore, translation continues through the intron, giving rise to the C-terminal protein region from amino acid residues ~~408 to 461~~ 102-155 of SEQ ID NO: 17. The region of 3' untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide ~~1469 to 1804~~ 650-887 of SEQ ID NO 16.

**Please amend the paragraph beginning on page 45, line 30, as follows:**

pEF-FLAG was generated by modifying the expression vector pEF-BOS as follows:-  
pEF-BOS (16) was digested with Xba I and a linker was synthesized that encoded the mouse IL3 signal sequence (MVLASSTTSIHTMLLLLLMLFHLGLQASIS)(SEQ ID NO: 32) and the FLAG epitope (DYKDDDDK)(SEQ ID NO: 55). *Asc* I and *Mlu* I restriction enzyme sites were also introduced as cloning sites.

The sequence of the linker is as follows:-

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                M V L A S S T T S I H T M
5'   CTAGACTAGTGCTGACACAATGGTTCTTGCCAGCTCTACCACCAGCATCCACACCATG
3'   TGATCACGACTGTGTTACCAAGAACGGTCGAGATGGTGGTCGTAGGTGTGGTAC

    L L L L L M L F H L G L Q A S I S (SEQ ID NO: 32)
                                Asc I
CTGCTCCTGCTCCTGATGCTCTTCCACCTGGGACTCCAAGCTTCAATCTCGGCGCGCC
GACGAGGACGAGGACTAGCAGAAGGTGGACCCTGAGGTTCGAAGTTAGAGCCGCGCGG

    D Y K D D D D K (SEQ ID NO: 55)
                        Mlu I
AGGACTACAAGGACGACGATGACAAGACGCGTGCTAGCACTAGT 3' (SEQ ID NO: 56)
TCCTGATGTTCCCTGCTGCTACTGTTCTGCGCACGATCGTGATCAGATC 5' (SEQ ID NO: 57)

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The two oligonucleotides (SEQ ID NOS: 56 and 57) were annealed together and ligated into the Xba I site of pEF-BOS to give pEF-FLAG.